



Figure S2. Genomic content across strains. (A) Sequence coverage was used to determine the genomic contribution of sequences from the *Saccharomyces sensu stricto* group in each strain. Each tile represents one of the sixteen chromosomes of each species, except for the *S. cerevisiae* sequence set which also contains 26 strain-variable accessory (pan-genome) loci. Strains are ordered according to the genome-wide SNP phylogeny and colored according to clade (ale, red; wine, blue and green; PdM, dark green, VIN7, light green). (B) A detailed display of the *S. cerevisiae* accessory elements of the pan-genome.